SEQUENCE LISTING

- (1) GENERAL INFORMATION:
 - (i) APPLICANT: Lyman, Stewart D.

 Beckmann, M. Patricia
 - (ii) TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
 - (iii) NUMBER OF SEQUENCES: 8
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Stephen L. Malaska, Immunex Corporation
 - (B) STREET: 51 University Street
 - (C) CITY: Seattle
 - (D) STATE: Washington
 - (E) COUNTRY: US
 - (F) ZIP: 98101
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: Apple Macintosh
 - (C) OPERATING SYSTEM: Macintosh 7.0.1
 - (D) SOFTWARE: Microsoft Word, Version #5.1
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: -to be assigned-
 - (B) FILING DATE: December 3, 1993
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/111,758
 - (B) FILING DATE: August 25, 1993
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/106,463
 - (B) FILING DATE: August 12, 1993
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/068,394
 - (B) FILING DATE: May 24, 1993
 - (C) CLASSIFICATION:
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Malaska, Stephen L.
 - (B) REGISTRATION NUMBER: 32,655
 - (C) REFERENCE/DOCKET NUMBER: 2813-C
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (206) 587-0430
 - (B) TELEFAX: (206) 233-0644
 - (C) TELEX: 756822
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 879 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION: $1..2\overline{5}$
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 (B) LOCATION: 855..879
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 57..752
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTC	SACTO	GGA A	ACGAC	GACGA	AC CI	rgcto	CTGTC	ACA	AGGC	ATGA	GGG	STCC	CCG (GCAG!	AG	56
						GCC Ala										104
						CCT Pro										152
						TCC Ser										200
_	_				_	AAA Lys 55	_	_								248
						TGC Cys			_							296
						CTG Leu										344
						AAC Asn										392
						GAA Glu										440

		CTC Leu		_												488
		GGG Gly	-													536
		CCG Pro												_	_	584
		GCC Ala														632
	-	CTG Leu 195	_				_			-						680
		CGC Arg														728
		CTC Leu					TAG	SATT(CGA (GCCT'	rgtgo	CA TO	CGTT	GACT	2	779
AGC	CAGG	GTC :	TAT	CTCG	эт та	ACAC	CTGT	A ATO	CTCA	GCCC	TTG	GGAG	CCC I	AGAG	CAGGAT	839
TGC	rgaa:	rgg :	CTG	GAGC	AG G	CGT	CTCG:	r TC	CAGT	CGAC						879

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 231 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Val Leu Ala Pro Ala Trp Ser Pro Asn Ser Ser Leu Leu Leu 1 5 10 15

Leu Leu Leu Leu Ser Pro Cys Leu Arg Gly Thr Pro Asp Cys Tyr 20 25 30

Phe Ser His Ser Pro Ile Ser Ser Asn Phe Lys Val Lys Phe Arg Glu 35 40 45

Leu Thr Asp His Leu Leu Lys Asp Tyr Pro Val Thr Val Ala Val Asn 50 55 60

Leu Gln Asp Glu Lys His Cys Lys Ala Leu Trp Ser Leu Phe Leu Ala 65 70 75 80

Gln Arg Trp Ile Glu Gln Leu Lys Thr Val Ala Gly Ser Lys Met Gln 85 90 95

Thr Leu Leu Glu Asp Val Asn Thr Glu Ile His Phe Val Thr Ser Cys 100 105 110

Thr Phe Gln Pro Leu Pro Glu Cys Leu Arg Phe Val Gln Thr Asn Ile 115 120 125

Ser His Leu Leu Lys Asp Thr Cys Thr Gln Leu Leu Ala Leu Lys Pro 130 135 140

Cys Ile Gly Lys Ala Cys Gln Asn Phe Ser Arg Cys Leu Glu Val Gln 145 150 155 160

Cys Gln Pro Asp Ser Ser Thr Leu Leu Pro Pro Arg Ser Pro Ile Ala 165 170 175

Leu Glu Ala Thr Glu Leu Pro Glu Pro Arg Pro Arg Gln Leu Leu Leu 180 185 190

Leu Leu Leu Leu Pro Leu Thr Leu Val Leu Leu Ala Ala Trp
195 200 205

Gly Leu Arg Trp Gln Arg Ala Arg Arg Gly Glu Leu His Pro Gly 210 215 220

Val Pro Leu Pro Ser His Pro 225 230

- (2) INFORMATION FOR SEQ ID NO:3:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCGACTGGAA CGAGACGACC TGCT

24

- (2) INFORMATION FOR SEQ ID NO:4:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO

(XI) DECORRED DESCRIPTION. DEC 10 NO.3	(xi)	SEOUENCE	DESCRIPTION:	SEO	ID	NO:4
--	------	----------	--------------	-----	----	------

AGCA	GGTC	GT (CTCGI	TCC	\G									20
(2)	INFO	RMAI	NOI	FOR	SEQ	ID N	10:5:	:						
	(i)	(E	A) LE 3) TY C) ST	ENGTH (PE: TRAND	ARAC H: 98 nucl DEDNE DGY:	88 ba eic ESS:	se p acio sino	oairs 1	3					
	(ii)	MOI	LECUI	LE TY	PE:	cDNA	A to	mRN/	Ą					
,	(iii)	НҮЕ	РОТНЕ	ETICA	AL: N	10								
	(iv)	NA C	rı-sı	ENSE:	NO									
		(E	A) NA B) LO	AME/F	KEY:	30		SEO I	ID NO	.				
		SEÇ	-					_			ama	~~~	 	.
CGGG	CGGA	AAT 1	rccgc	3GGC(ce ee	CGGCC	CGAA						Ala	53
		ACA Thr												101
		ACC Thr												149
		GTC Val												197
		ACC Thr												245
		CGG Arg 75												293
		GGG Gly												341
		TTT Phe												389
		GTC Val												437

														TCC Ser		485
														CCC Pro		533
														CAG Gln		581
														CTG Leu		629
														CCC Pro 215		677
														CTG Leu		725
	GAG Glu		TGA	CCTG	GCC P	AAGGO	CCTC	AT CO	CTGC	GGAG	C CT	ГАААС	CAAC			774
GCA	GTGAC	SAC A	AGAC	ATCTA	AT C	ATCC	CATT	TAC	CAGG	GGAG	GATA	ACTG	AGG (CACAC	CAGAGG	834
GGA	GTCAC	CCA (GCCA	GAGG	AT GI	CATAC	GCCT	G GA	CACAC	GAGG	AAG:	TGGC	CTA (GAGG	CCGGTC	894
CCT	гсстт	rgg (SCCC	CTCT	CA TI	rccci	rccco	C AGA	AATGO	GAGG	CAA	CGCCZ	AGA A	ATCC	AGCACC	954
GGC	CCCAT	TTT A	ACCC	AACTO	CT G	AACAA	AAGCO	c cc	CG							988

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 235 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu 1 5 10 15

Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
20 25 30

Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu 35 40 45

Ser Asp Tyr Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu 50 60

Gln 65	Asp	Glu	Glu	Leu	Cys 70	Gly	Gly	Leu	Trp	Arg 75	Leu	Val	Leu	Ala	Gln 80	
Arg	Trp	Met	Glu	Arg 85	Leu	Lys	Thr	Val	Ala 90	Gly	Ser	Lys	Met	Gln 95	Gly	
Leu	Leu	Glu	Arg 100	Val	Asn	Thr	Glu	Ile 105	His	Phe	Val	Thr	Lys 110	Cys	Ala	
Phe	Gln	Pro 115	Pro	Pro	Ser	Cys	Leu 120	Arg	Phe	Val	Gln	Thr 125	Asn	Ile	Ser	
Arg	Leu 130	Leu	Gln	Glu	Thr	Ser 135	Glu	Gln	Leu	Val	Ala 140	Leu	Lys	Pro	Trp	
Ile 145	Thr	Arg	Gln	Asn	Phe 150	Ser	Arg	Cys	Leu	Glu 155	Leu	Gln	Cys	Gln	Pro 160	
Asp	Ser	Ser	Thr	Leu 165	Pro	Pro	Pro	Trp	Ser 170	Pro	Arg	Pro	Leu	Glu 175	Ala	
Thr	Ala	Pro	Thr 180	Ala	Pro	Gln	Pro	Pro 185	Leu	Leu	Leu	Leu	Leu 190	Leu	Leu	
Pro	Val	Gly 195	Leu	Leu	Leu	Leu	Ala 200	Ala	Ala	Trp	Cys	Leu 205	His	Trp	Gln	
Arg	Thr 210	Arg	Arg	Arg	Thr	Pro 215	Arg	Pro	Gly	Glu	Gln 220	Val	Pro	Pro	Val	
Pro 225	Ser	Pro	Gln	Asp	Leu 230	Leu	Leu	Val	Glu	His 235						
(2)	INF	ORMA!	rion	FOR	SEQ	ID 1	10:7	:								
	(i)	(1 (1	A) L1 B) T1 C) S1	CE CI ENGTI YPE: TRANI OPOLO	H: 7: nuc: DEDNI	l bas leic ESS:	se pa acio sino	airs d								
	(ii)) MO	LECU:	LE T	YPE:	cDN	A to	mRN	Ą							
	(iii	HYI	РОТН	ETIC	AL: 1	10										
	(iv) AN'	ri-si	ENSE	: NO											
	(xi) SE	QUEN	CE D	ESCR:	IPTI	ON:	SEQ :	ID N	0:7:						
AAT	TGGT	ACC '	TTTG	GATA.	AA A	GAGA	CTAC	A AG	GACG	ACGA	TGA	CAAG	ACA (CCTG	ACTGTT	60
ACT	TCAG	CCA (С													71

- (2) INFORMATION FOR SEQ ID NO:8:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
 ATATGGATCC CTACTGCCTG GGCCGAGGCT CTGGGAG

37

TRADEMARK

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lyman, Stewart D.

 Beckmann, M. Patricia
- (ii) TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Stephen L. Malaska, Immunex Corporation
 - (B) STREET: 51 University Street
 - (C) CITY: Seattle
 - (D) STATE: Washington
 - (E) COUNTRY: US
 - (F) ZIP: 98101
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: Apple Macintosh
 - (C) OPERATING SYSTEM: Macintosh 7.0.1
 - (D) SOFTWARE: Microsoft Word, Version #5.1
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: -to be assigned-
 - (B) FILING DATE: December 3, 1993
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/111,758
 - (B) FILING DATE: August 25, 1993
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/106,463
 - (B) FILING DATE: August 12, 1993
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/068,394
 - (B) FILING DATE: May 24, 1993
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Malaska, Stephen L.
 - (B) REGISTRATION NUMBER: 32,655
 - (C) REFERENCE/DOCKET NUMBER: 2813-C
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (206) 587-0430
 - (B) TELEFAX: (206) 233-0644
 - (C) TELEX: 756822
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 879 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..25

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 855..879

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 57..752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCGACTGGA ACGAGA	ACGAC CTGCTCTGTC AC	AGGCATGA GGGG	TCCCCG GCAGAG	56
Met Thr Val Leu A	GCG CCA GCC TGG AGC la Pro Ala Trp Ser 5			
	CTG AGT CCT TGC CTG Leu Ser Pro Cys Leu 25			
TTC AGC CAC AGT C	CCC ATC TCC TCC AAC Pro Ile Ser Ser Asn 40	Phe Lys Val	AAG TTT AGA G	
	CTG CTT AAA GAT TAC Leu Leu Lys Asp Tyr 55			
	AAG CAC TGC AAG GCC Lys His Cys Lys Ala 70		Leu Phe Leu A	
Gln Arg Trp Ile G	GAG CAA CTG AAG ACT Glu Gln Leu Lys Thr B5			
	GAC GTC AAC ACC GAG Asp Val Asn Thr Glu 105	lle His Phe		
	CTA CCA GAA TGT CTG Leu Pro Glu Cys Leu 120	Arg Phe Val		
	AAG GAC ACC TGC ACA Lys Asp Thr Cys Thr 135			

тст																
			AAG Lys													536
			GAC Asp													584
			ACG Thr 180													632
			CTG Leu													680
			TGG Trp													728
			CCC Pro				TAGO	GATT	CGA (GCCTI	rgtgo	CA TO	CGTT	GACTO		779
AGC	CAGG	STC 1	TATO	CTCGC	FT T2	ACACO	CTGT	TA A	CTCAC	SCCC	TTG	GAGO	CCC A	AGAGO	CAGGAT	839
TGC	rgaa:	rgg 1	CTG	GAGCA	AG GT	CGTC	CTCGT	r TCC	CAGTO	CGAC						879
(2)	INF	ORMAI	rion	FOR	SEQ	ID N	10:2	:								
		(i) S	SEQUE					rics:	1							
			(B)	TYE	E: a	amino SY:]	ac		acids	5						
	(±	Li) N	(B)	TYE TOE	POLOC	amino SY:]	o aci	id	acids	3						
		_	(B)	TYE TOE	PE: 6	amino GY:]	o aci	id ar in			2:					
Met 1	(2	(i) S	(B) (D) MOLEC	TYE TOE CULE	PE: 8 POLOG TYPE DESG	amino GY:] E: pi	o aci linea rotei	id ar in : SE() ID	NO:2		Ser	Leu	Leu 15	Leu	
1	(2 Thr	ki) S Val	(B) (D) MOLEC	TYF TOF CULE ENCE Ala	PE: & OLOG TYPE DESG	amino GY:] E: pr CRIPT	o aci linea rotei rion:	id ar in : SEÇ	Pro	NO:2	Ser			15		
1 Leu	(z Thr Leu	ki) S Val Leu	(B) (D) 40LEC SEQUE Leu	TYE TOE CULE ENCE Ala 5	PE: & POLOG TYPE DESG Pro	emino GY:] E: pr CRIPT Ala Pro	o actions cotes rion: Trp Cys	id ar in Ser Leu 25	Pro 10	NO:2 Asn Gly	Ser	Pro	Asp 30	15 Cys	Tyr	
1 Leu Phe	(z Thr Leu Ser	Val Leu His 35	(B) (D) MOLEC SEQUE Leu Leu 20	TYE TOE CULE ENCE Ala 5 Leu	PE: 8 POLOG TYPE DESG Pro Ser Ile	emind GY:] E: pr CRIPT Ala Pro	o actions rotes rion: Trp Cys Ser 40	id ar in Ser Leu 25	Pro 10 Arg	NO:2 Asn Gly Lys	Ser Thr Val	Pro Lys 45	Asp 30 Phe	15 Cys Arg	Tyr Glu	
1 Leu Phe Leu	Thr Leu Ser Thr 50	Val Leu His 35	(B) (D) MOLEC SEQUE Leu Leu 20 Ser	TYE TOE CULE ENCE Ala 5 Leu Pro	PE: & POLOG TYPE DESG Pro Ser Ile Leu	E: pr CRIPT Ala Pro Ser Lys 55	rion: Trp Cys Ser 40 Asp	id ar in Ser Leu 25 Asn	Pro 10 Arg Phe	NO:2 Asn Gly Lys Val	Ser Thr Val Thr 60	Pro Lys 45 Val	Asp 30 Phe	15 Cys Arg Val	Tyr Glu Asn	
1 Leu Phe Leu Leu 65	Thr Leu Ser Thr 50	val Leu His 35 Asp	(B) (D) (OLE) SEQUE Leu 20 Ser His	TYE TOE CULE ENCE Ala 5 Leu Pro Leu Lys	PE: 8 POLOG TYPE DESG Pro Ser Ile Leu His 70	E: pr CRIPT Ala Pro Ser Lys 55 Cys	o actioned from the content of the c	id ar in Ser Leu 25 Asn Tyr	Pro 10 Arg Phe Pro Leu	NO:2 Asn Gly Lys Val Trp 75	Ser Thr Val Thr 60	Pro Lys 45 Val Leu	Asp 30 Phe Ala	15 Cys Arg Val Leu	Tyr Glu Asn Ala 80	



Ser His Leu Leu Lys Asp Thr Cys Thr Gln Leu Leu Ala Leu Lys Pro 130 Cys Ile Gly Lys Ala Cys Gln Asn Phe Ser Arg Cys Leu Glu Val Gln 150 155 Cys Gln Pro Asp Ser Ser Thr Leu Leu Pro Pro Arg Ser Pro Ile Ala Leu Glu Ala Thr Glu Leu Pro Glu Pro Arg Pro Arg Gln Leu Leu Leu Leu Leu Leu Pro Leu Thr Leu Val Leu Leu Ala Ala Trp 200 Gly Leu Arg Trp Gln Arg Ala Arg Arg Arg Gly Glu Leu His Pro Gly 215 220 Val Pro Leu Pro Ser His Pro 225 230 (2) INFORMATION FOR SEQ ID NO:3: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: TCGACTGGAA CGAGACGACC TGCT 24 (2) INFORMATION FOR SEQ ID NO:4: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4: 20 AGCAGGTCGT CTCGTTCCAG (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 988 base pairs

Thr Phe Gln Pro Leu Pro Glu Cys Leu Arg Phe Val Gln Thr Asn Ile

((iii)	HYE	OTHE	TICA	L: N	10								
	(iv)	ANT	I-SE	NSE:	ИО									
	(ix)	(P	TURE A) NA B) LO	ME/K			734							
	(xi)	SEC	QUENC	E DE	SCRI	PTIC)N: S	SEQ 1	D NO	5:5:				
CGG(CCGGF	AT I	CCGG	GGCC	cc cc	CGGCC	GAA					CCA Pro		53
	CCA Pro 10													101
	GGG Gly													149
	GCT Ala													197
	GTC Val		-											245
	TGG Trp													293
	GCT Ala 90													341
	CAC His													389
	TTC Phe												_	437
	CTG Leu													485
	CTG Leu		-											533

(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

				CCC Pro												581
				CTA Leu												629
				CTG Leu 205												677
				GTG Val												725
	GAG Glu		TGA	CCTG	GCC 1	AAGG(CCTC	AT CO	CTGC	GGAG	C CT	(ААА	CAAC			774
GCA	GTGA	GAC A	AGAC	ATCTA	AT C	ATCC	CATT	TA(CAGG	GGAG	GAT	ACTG	AGG (CACA	CAGAGG	834
GGA	GTCA	CCA (GCCA	GAGG	AT G	rata(GCCT	G GA	CACA	GAGG	AAG'	rtgg	CTA (GAGG	CCGGTC	894
CCT	CCT'	rgg (GCCC	CTCT	CA T	rccc	rccc	CAG	AATG	GAGG	CAA	CGCC	AGA A	ATCC2	AGCACC	954
GGC	CCA	TTT 2	ACCC	AACT	CT G	AACA	AAGC	c cc	CG							988
(2)	INF	ORMA'	rion	FOR	SEQ	ID 1	10:6	:								
		153	20011													
		(1)	(A)	ENCE) LEI) TYI) TOI	NGTH PE: a	: 239 amin	5 am	id		3						-
			(A) (B) (D)) LEI) TYI	NGTH PE: 8 POLO	: 235 amino GY: 3	5 am: o ac: linea	ino a id ar		5						-
	(:	ii) I	(A) (B) (D)) LEI) TYI) TOI	NGTH PE: 8 POLOG	: 23: amino GY: :	5 am: o ac: linea	ino a id ar in	acid		ó :					-
Met 1	(:	ii) I	(A) (B) (D) MOLEG) LEI) TYI) TOI CULE	NGTH PE: 6 POLOG TYPI DESG	: 23: amino GY: : E: p: CRIP!	5 ams 5 acs 1inea rotes	ino a id ar in : SE	acid: Q ID	NO:		Tyr	Leu	Leu 15	Leu	٠
1	(: (: Thr	ii) ! ki) ! Val	(A) (B) (D) MOLE SEQUI) LEM) TYM) TOM CULE ENCE Ala	NGTH PE: 6 POLOG TYP1 DESG	: 239 amino GY: 1 E: p: CRIP: Ala	5 ams 5 ams 6 acs	ino a id ar in : SEG	Q ID Pro 10	NO:	Thr	_		15		
1 Leu	(: Thr Leu	ii) ! ki) : Val Leu	(A) (B) (D) MOLE SEQUI) LENCE Ala 5	NGTH PE: 2 POLOG TYPI DESG Pro	: 23: amino GY: : E: p: CRIP! Ala Gly	5 ams 5 acs 6 acs 6 acs 7 inea 7 inea 7 inea 7 inea 7 inea 7 inea 8 inea	ino a id ar in Ser Ser 25	Q ID Pro 10	NO:0	Thr	Asp	Cys 30	15 Ser	Phe	
1 Leu Gln	(: Thr Leu His	ii) ! ki) : Val Leu Ser 35	(A) (B) (D) MOLEG SEQUI Leu Leu 20 Pro) LEI) TYI) TOI CULE ENCE Ala 5	NGTH PE: 8 POLOG TYPI DESG Pro Ser	: 23: amino GY: : E: p: CRIP! Ala Gly Ser	5 ams c acs linea rotes TION Trp Leu Asp 40	ino aid ar in Ser Ser 25	Q ID Pro 10 Gly Ala	NO:6 Thr Thr	Thr Gln Lys	Asp Ile 45	Cys 30 Arg	15 Ser Glu	Phe Leu	
1 Leu Gln Ser	(: Thr Leu His Asp	ii) I ki) S Val Leu Ser 35	(A) (B) (D) MOLEO SEQUI Leu 20 Pro) LED) TYI) TOI CULE ENCE Ala 5 Ser	TYPI DESC Pro Ser Ser	: 23: amino GY: : E: p: CRIP! Ala Gly Ser Asp 55	5 ams 5 acs 6 acs 6 inea 7 ION 7 Trp Leu Asp 40 Tyr	ino a id ar in Ser Ser 25 Phe	Q ID Pro 10 Gly Ala	NO:0 Thr Thr Val	Thr Gln Lys Val 60	Asp Ile 45 Ala	Cys 30 Arg Ser	15 Ser Glu Asn	Phe Leu Leu	
1 Leu Gln Ser Gln 65	(: Thr Leu His Asp 50	ii) ! ki) : Val Leu Ser 35 Tyr	(A) (B) (D) MOLEG SEQUI Leu 20 Pro Leu Glu) LEI) TYI) TOI CULE ENCE Ala 5 Ser Ile	NGTH PE: 3 POLOO TYPI DESO Pro Ser Ser Gln Cys 70	: 23! amino GY: : CRIP! Ala Gly Ser Asp 55 Gly	o amico accidines rote: TION Trp Leu Asp 40 Tyr Gly	ino aid ar in SEG Ser 25 Phe Pro	Q ID Pro 10 Gly Ala Val	NO:0 Thr Thr Val Thr Arg 75	Thr Gln Lys Val 60 Leu	Asp Ile 45 Ala Val	Cys 30 Arg Ser	15 Ser Glu Asn	Phe Leu Leu Gln 80	

Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser 120 Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp 130 135 Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro 150 155 Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu Leu Leu Leu Leu Leu 185 Pro Val Gly Leu Leu Leu Ala Ala Trp Cys Leu His Trp Gln 200 Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly Glu Gln Val Pro Pro Val 215 Pro Ser Pro Gln Asp Leu Leu Leu Val Glu His 230 (2) INFORMATION FOR SEQ ID NO:7: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 71 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7: AATTGGTACC TTTGGATAAA AGAGACTACA AGGACGACGA TGACAAGACA CCTGACTGTT 71 ACTTCAGCCA C (2) INFORMATION FOR SEQ ID NO:8: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 37 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
ATATGGATCC CTACTGCCTG GGCCGAGGCT CTGGGAG

37